GenCore version 4.5

OM protein - protein search, using sw model

Run on: July 12, 2002, 14:19:56 ; Search time 23.81 Seconds
(without alignments)
29.063 Million cell updates/sec

Title: US-09-807-980-1
Perfect score: 24
Sequence: 1 GGFG 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 378

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : SPTREMBL_19:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*

16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	13	54.2	7	10	O49223	O49223 glycine max
2	12	50.0	5	13	P82073	P82073 litoria rub
3	12	50.0	7	11	Q63480	Q63480 rattus norv
4	12	50.0	7	11	O55184	O55184 rattus norv
5	12	50.0	8	4	Q9P0K3	Q9p0k3 homo sapien
6	12	50.0	8	4	Q15901	Q15901 homo sapien
7	12	50.0	8	4	Q96RN9	Q96rn9 homo sapien
8	12	50.0	8	4	Q96Q65	Q96q65 homo sapien
9	12	50.0	8	11	Q9QVI5	Q9qvi5 rattus sp.
10	12	50.0	8	11	Q9R1U6	Q9r1u6 mus musculu
11	12	50.0	8	13	P82079	P82079 limnodynast
12	11	45.8	8	6	Q9TT78	Q9tt78 canis famil
13	11	45.8	8	8	P92386	P92386 hordeum mar
14	9	37.5	8	2	Q9R5R2	Q9r5r2 shigella dy
15	9	37.5	8	2	O09258	O09258 synechococc
16	9	37.5	8	2	O85406	O85406 coxiella bu
17	9	37.5	8	7	Q95213	Q95213 oryctolagus
18	8	33.3	8	8	P92422	P92422 psathyrosta
19	8	33.3	8	8	P92373	P92373 haynaldia v
20	8	33.3	8	8	P93985	P93985 aegilops co
21	8	33.3	8	8	P92404	P92404 lophopyrum
22	8	33.3	8	8	P92426	P92426 pseudoroegn
23	8	33.3	8	8	P93973	P93973 eremopyrum
24	8	33.3	8	8	P93970	P93970 eremopyrum
25	8	33.3	8	8	P92388	P92388 henrardia p
26	8	33.3	8	8	P92428	P92428 peridictyon
27	8	33.3	8	8	P92391	P92391 heteranthel
28	8	33.3	8	8	P92227	P92227 crithopsis
29	8	33.3	8	8	P93963	P93963 psathyrosta
30	8	33.3	8	8	P93961	P93961 psathyrosta
31	8	33.3	8	8	P92215	P92215 amblyopyrum
32	8	33.3	8	8	P93981	P93981 crithodium
33	8	33.3	8	8	P92431	P92431 aegilops ta

34 8 33.3 8 8 P92222 P92222 bromus iner
ALIGNMENTS

RESULT 1
O49223
ID O49223 PRELIMINARY; PRT; 7 AA.
AC O49223;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HMG-1-LIKE PROTEIN (FRAGMENT).
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. ESSEX; TISSUE=ROOT;
RX MEDLINE=91367679; PubMed=1891369;
RA Laux T., Goldberg R.B.;
RT "A plant DNA binding protein shares highly conserved sequence motifs
RT with HMG-box proteins.";
RL Nucleic Acids Res. 19:4769-4769(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. ESSEX; TISSUE=ROOT;
RA Mahalingam R., Knap H.T.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF047050; AAC03556.1; -.
FT NON_TER 1 1
SQ SEQUENCE 7 AA; 850 MW; 6AAAAAB378637810 CRC64;

Query Match 54.2%; Score 13; DB 10; Length 7;
Best Local Similarity 66.7%; Pred. No. 5.6e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GFG 4
|:|
Db 1 GWG 3
Search completed: July 12, 2002, 14:23:24
Job time: 208 sec

GenCore version 4.5

OM protein - protein search, using sw model

Run on: July 12, 2002, 14:20:12 ; Search time 10.15 Seconds
(without alignments)
15.259 Million cell updates/sec

Title: US-09-807-980-1
Perfect score: 24
Sequence: 1 GGFG 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 148

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	18	75.0	4	1	OCP1_OCTMI	P58648 octopus min
2	12.5	52.1	8	1	ALL9_CARMA	P81812 carcinus ma
3	12	50.0	4	1	ACH1_ACHFU	P35904 achatina fu
4	12	50.0	5	1	AL14_CARMA	P81817 carcinus ma
5	12	50.0	5	1	PAP2_PARMA	P81864 pardachirus

6	12	50.0	5	1	RE32_LITRU	P82073 litoria rub
7	12	50.0	6	1	FARP_MONEX	P41966 moniezia ex
8	12	50.0	7	1	ALL2_CARMA	P81805 carcinus ma
9	12	50.0	7	1	ALL3_CARMA	P81806 carcinus ma
10	12	50.0	7	1	ALL4_CARMA	P81807 carcinus ma
11	12	50.0	7	1	ALL5_CARMA	P81808 carcinus ma
12	12	50.0	7	1	ALL7_CYDPO	P82158 cydia pomon
13	12	50.0	7	1	FAR5_HIRME	P42564 hirudo medi
14	12	50.0	8	1	AL12_CARMA	P81815 carcinus ma
15	12	50.0	8	1	AL15_CARMA	P81818 carcinus ma
16	12	50.0	8	1	AL16_CARMA	P81819 carcinus ma
17	12	50.0	8	1	AL17_CARMA	P81820 carcinus ma
18	12	50.0	8	1	AL18_CARMA	P81821 carcinus ma
19	12	50.0	8	1	ALL1_CYDPO	P82152 cydia pomon
20	12	50.0	8	1	ALL3_CYDPO	P82154 cydia pomon
21	12	50.0	8	1	ALL4_CALVO	P41840 calliphora
22	12	50.0	8	1	ALL4_CYDPO	P82155 cydia pomon
23	12	50.0	8	1	ALL5_CALVO	P41841 calliphora
24	12	50.0	8	1	ALL5_CYDPO	P82156 cydia pomon
25	12	50.0	8	1	ALL6_CYDPO	P82157 cydia pomon
26	12	50.0	8	1	ALL7_CARMA	P81809 carcinus ma
27	12	50.0	8	1	ALL8_CARMA	P81811 carcinus ma
28	12	50.0	8	1	LCK2_LEUMA	P21141 leucophaea
29	12	50.0	8	1	LCK3_LEUMA	P21142 leucophaea
30	12	50.0	8	1	LCK5_LEUMA	P19987 leucophaea
31	12	50.0	8	1	ORMY_ORCLI	P82455 orconectes
32	12	50.0	8	1	UF06_MOUSE	P38644 mus musculu
33	11	45.8	8	1	LMT2_LOCMI	P22396 locusta mig
34	10	41.7	8	1	VGLG_HSV2B	P81780 herpes simp
35	9	37.5	7	1	UN06_PINPS	P81675 pinus pinas
36	7	29.2	4	1	OCP3_OCTMI	P58649 octopus min
37	7	29.2	6	1	LOK1_LOCMI	P41491 locusta mig
38	7	29.2	8	1	ACI_THUAL	P18691 thunnus alb
39	7	29.2	8	1	AKHG_GRYBI	P14086 gryllus bim
40	7	29.2	8	1	AKH_TABAT	P14595 tabanus atr
41	7	29.2	8	1	CCKN_MACEU	P30369 macropus eu
42	7	29.2	8	1	LCK1_LEUMA	P21140 leucophaea
43	7	29.2	8	1	LCK4_LEUMA	P21143 leucophaea
44	7	29.2	8	1	LCK6_LEUMA	P19988 leucophaea
45	7	29.2	8	1	LCK7_LEUMA	P19989 leucophaea
46	7	29.2	8	1	LCK8_LEUMA	P19990 leucophaea
47	7	29.2	8	1	RPCH_PANBO	P08939 pandalus bo
48	6	25.0	3	1	GRWM_HUMAN	P01157 homo sapien
49	6	25.0	4	1	DCML_PSECH	P19916 pseudomonas
50	6	25.0	4	1	EOSI_HUMAN	P02731 homo sapien

ALIGNMENTS

RESULT 1
OCP1_OCTMI
ID OCP1_OCTMI STANDARD; PRT; 4 AA.
AC P58648;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Cardioactive peptides Ocp-1/Ocp-2.
OS Octopus minor (Octopus).
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Octopoda;
OC Incirrata; Octopodidae; Octopus.
OX NCBI_TaxID=89766;
RN [1]
RP SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.
RC TISSUE=Brain;
RX PubMed=10876044;
RA Iwakoshi E., Hisada M., Minakata H.;
RT "Cardioactive peptides isolated from the brain of a Japanese octopus,
RT Octopus minor.";
RL Peptides 21:623-630(2000).
CC -!- FUNCTION: Cardioactive; has both positive chronotropic and
CC inotropic effects on the heart. Ocp-2 is a 1000 time less
CC active than Ocp-1.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PTM: Ocp-2 has L-Phe instead of D-Phe.
CC -!- MASS SPECTROMETRY: MW=395.2; METHOD=MALDI.
KW Hormone; D-amino acid.
FT MOD_RES 2 2 D-PHENYLALANINE.
SQ SEQUENCE 4 AA; 394 MW; 6AA879C810000000 CRC64;

Query Match 75.0%; Score 18; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GFG 4
|||
Db 1 GFG 3

Search completed: July 12, 2002, 14:23:36
Job time: 204 sec

GenCore version 4.5

OM protein - protein search, using sw model

Run on: July 12, 2002, 14:19:21 ; Search time 14.14 Seconds
(without alignments)
27.182 Million cell updates/sec

Title: US-09-807-980-1
Perfect score: 24
Sequence: 1 GGFG 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 603

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	DB	ID	Description
1	18	75.0	5	2	B61445	Leu-enkephalin - b

2	18	75.0	5	2	A61445	Met-enkephalin - b
3	18	75.0	5	2	B61168	cocoonase (EC 3.4.
4	18	75.0	6	2	PT0727	T-cell receptor be
5	18	75.0	7	2	A60224	Met-enkephalin-Arg
6	18	75.0	8	2	PC4373	telomeric and tetr
7	15	62.5	6	2	PT0514	T-cell receptor be
8	15	62.5	8	2	PH1618	Ig H chain V-D-J r
9	12	50.0	3	3	A23751	spinal cord peptid
10	12	50.0	4	2	A32480	achatin-I - giant
11	12	50.0	4	2	A53284	T-cell receptor be
12	12	50.0	4	2	B53284	T-cell receptor be
13	12	50.0	4	2	PT0706	T-cell receptor be
14	12	50.0	4	2	S47552	ubiquitin - rat
15	12	50.0	5	2	A44955	alkanal monooxygen
16	12	50.0	5	2	JH0253	gut pentapeptide -
17	12	50.0	5	2	PT0267	Ig heavy chain CRD
18	12	50.0	5	2	PT0278	Ig heavy chain CRD
19	12	50.0	5	2	C53284	T-cell receptor be
20	12	50.0	5	2	PT0669	T-cell receptor be
21	12	50.0	5	2	PT0707	T-cell receptor be
22	12	50.0	5	2	PT0585	T-cell receptor be
23	12	50.0	5	2	PT0717	T-cell receptor be
24	12	50.0	6	2	JU0355	lipopeptide WS1279
25	12	50.0	6	2	PT0629	T-cell receptor be
26	12	50.0	6	2	PT0512	T-cell receptor be
27	12	50.0	6	2	PT0643	T-cell receptor be
28	12	50.0	6	2	PT0605	T-cell receptor be
29	12	50.0	6	2	PT0720	T-cell receptor be
30	12	50.0	6	2	PT0560	T-cell receptor be
31	12	50.0	6	2	PT0723	T-cell receptor be
32	12	50.0	6	2	PT0718	T-cell receptor be
33	12	50.0	6	2	PT0730	T-cell receptor be
34	12	50.0	6	2	A41946	T-cell receptor ga
35	12	50.0	6	2	A43129	neuropeptide GNFFR
36	12	50.0	7	1	A61324	dermorphin - Rohde
37	12	50.0	7	2	S36662	dermorphin (Lys-7)
38	12	50.0	7	2	S42407	gramicidin S synth
39	12	50.0	7	2	I40504	hypothetical prote
40	12	50.0	7	2	T09512	NADH dehydrogenase
41	12	50.0	7	2	E61491	seed protein ws-5
42	12	50.0	7	2	H33098	180K exoantigen -
43	12	50.0	7	2	PT0529	T-cell receptor be
44	12	50.0	7	2	PT0523	T-cell receptor be
45	12	50.0	7	2	PT0642	T-cell receptor be
46	12	50.0	7	2	PT0667	T-cell receptor be

ALIGNMENTS

RESULT 1
B61445
Leu-enkephalin - blue mussel
C;Species: Mytilus edulis (blue mussel)
C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 21-Jan-2000
C;Accession: B61445
R;Leung, M.K.; Stefano, G.B.
Proc. Natl. Acad. Sci. U.S.A. 81, 955-958, 1984
A;Title: Isolation and identification of enkephalins in pedal ganglia of Mytilus edulis (Mollusca).
A;Reference number: A61445; MUID:84144823
A;Accession: B61445
A;Molecule type: protein
A;Residues: 1-5 <LEU>
A;Experimental source: pedal ganglia
C;Keywords: neuropeptide; opioid peptide

Query Match 75.0%; Score 18; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGF 3
|||
Db 2 GGF 4

Search completed: July 12, 2002, 14:20:07
Job time: 46 sec

GenCore version 4.5

OM protein - protein search, using sw model

Run on: July 12, 2002, 14:19:21 ; Search time 12.87 Seconds
(without alignments)
7.591 Million cell updates/sec

Title: US-09-807-980-1
Perfect score: 24
Sequence: 1 GGFG 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 48605

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description

1	24	100.0	4	2	US-08-689-018-3	Sequence 3, Appli
2	24	100.0	4	5	PCT-US96-00888-1	Sequence 1, Appli
3	24	100.0	5	4	US-08-842-306B-20	Sequence 20, Appl
4	24	100.0	5	4	US-08-838-973B-18	Sequence 18, Appl
5	24	100.0	6	1	US-07-718-577-12	Sequence 12, Appl
6	24	100.0	6	1	US-08-291-368-19	Sequence 19, Appl
7	24	100.0	6	2	US-08-962-190-19	Sequence 19, Appl
8	24	100.0	6	5	PCT-US95-10310-19	Sequence 19, Appl
9	19	79.2	6	1	US-07-973-235A-20	Sequence 20, Appl
10	19	79.2	6	2	US-08-462-720-20	Sequence 20, Appl
11	18	75.0	3	2	US-09-060-455-2	Sequence 2, Appli
12	18	75.0	4	1	US-07-822-924-5	Sequence 5, Appli
13	18	75.0	4	1	US-07-796-243-3	Sequence 3, Appli
14	18	75.0	4	1	US-07-805-727-15	Sequence 15, Appl
15	18	75.0	4	1	US-07-969-307A-1	Sequence 1, Appli
16	18	75.0	4	1	US-07-969-307A-2	Sequence 2, Appli
17	18	75.0	4	1	US-07-969-307A-3	Sequence 3, Appli
18	18	75.0	4	1	US-08-076-726-4	Sequence 4, Appli
19	18	75.0	4	1	US-08-257-782-36	Sequence 36, Appl
20	18	75.0	4	1	US-07-980-523-3	Sequence 3, Appli
21	18	75.0	4	1	US-08-488-470A-1	Sequence 1, Appli
22	18	75.0	4	1	US-08-577-846-36	Sequence 36, Appl
23	18	75.0	4	1	US-07-946-239-10	Sequence 10, Appl
24	18	75.0	4	1	US-08-484-505A-1	Sequence 1, Appli
25	18	75.0	4	2	US-08-530-277-3	Sequence 3, Appli
26	18	75.0	4	2	US-08-530-277-5	Sequence 5, Appli
27	18	75.0	4	2	US-08-530-277-7	Sequence 7, Appli
28	18	75.0	4	2	US-08-453-958-1	Sequence 1, Appli
29	18	75.0	4	2	US-08-514-451A-16	Sequence 16, Appl
30	18	75.0	4	2	US-08-249-830-2	Sequence 2, Appli
31	18	75.0	4	2	US-08-070-301-4	Sequence 4, Appli
32	18	75.0	4	2	US-08-740-170-3	Sequence 3, Appli
33	18	75.0	4	2	US-08-685-589A-70	Sequence 70, Appl
34	18	75.0	4	2	US-08-687-702-23	Sequence 23, Appl
35	18	75.0	4	2	US-08-687-702-27	Sequence 27, Appl
36	18	75.0	4	2	US-08-747-137-123	Sequence 123, App
37	18	75.0	4	2	US-08-747-137-125	Sequence 125, App
38	18	75.0	4	2	US-09-060-455-14	Sequence 14, Appl
39	18	75.0	4	3	US-09-327-424-1	Sequence 1, Appli
40	18	75.0	4	3	US-08-383-766-5	Sequence 5, Appli
41	18	75.0	4	3	US-09-198-209-2	Sequence 2, Appli
42	18	75.0	4	3	US-08-963-168C-20	Sequence 20, Appl
43	18	75.0	4	4	US-09-090-793-33	Sequence 33, Appl
44	18	75.0	4	4	US-09-151-467-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-08-689-018-3
; Sequence 3, Application US/08689018
; Patent No. 5837673
; GENERAL INFORMATION:
; APPLICANT: TSUJIHARA, KENJI
; APPLICANT: KAWAGUCHI, TAKAYUKI
; APPLICANT: OKUNO, SATOSHI
; APPLICANT: YANO, TOSHIRO
; TITLE OF INVENTION: CAMPTOTHECIN DERIVATIVES
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
; STREET: 8110 GATEHOUSE RD.
; CITY: FALLS CHURCH
; STATE: VIRGINIA
; COUNTRY: UNITED STATES
; ZIP: 22042
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/689,018
; FILING DATE: 30-JUL-1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: SVENSSON, LEONARD R
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 20-4049
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)205-8000
; TELEFAX: (703)205-8050
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-689-018-3

Query Match 100.0%; Score 24; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 GGFG 4
          ||||
Db      1 GGFG 4
```

Search completed: July 12, 2002, 14:19:54
Job time: 33 sec

GenCore version 4.5

OM protein - protein search, using sw model

Run on: July 12, 2002, 14:19:21 ; Search time 28.9 Seconds
(without alignments)
15.374 Million cell updates/sec

Title: US-09-807-980-1
Perfect score: 24
Sequence: 1 GGFG 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 69368

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	24	100.0	4	17	AAR99475	Encoded reaction c
2	24	100.0	4	20	AAY04398	Spacer peptide #1.
3	24	100.0	4	21	AAY91118	Drug delivery syst
4	24	100.0	4	21	AAY49436	Spacer peptide mol
5	24	100.0	5	20	AAY04402	Spacer peptide #5.
6	24	100.0	5	21	AAB03528	Drug delivery syst
7	24	100.0	5	22	AAG65469	Conserved region o
8	24	100.0	6	16	AAR80649	Receptor binding p
9	24	100.0	6	17	AAR89489	CryIF class toxin
10	24	100.0	8	19	AAW54524	High affinity Kb b
11	21	87.5	7	19	AAW70512	Escherichia coli g
12	21	87.5	7	20	AAY33390	A. diadematus fibr
13	21	87.5	7	22	AAU09037	Silk spider fibroi
14	19	79.2	6	13	AAR20416	Anti-b-endorphin m
15	19	79.2	6	15	AAR55080	Fibronectin gelati
16	19	79.2	6	16	AAR69786	Thrombospondin-der
17	19	79.2	6	22	AAB86433	T. thermophila tri
18	19	79.2	8	19	AAW69140	Neuronal NOS bindi
19	19	79.2	8	21	AAB07319	Mammalian prion pr
20	19	79.2	8	21	AAB07330	Mammalian prion pr
21	18	75.0	4	2	AAP10380	Enkephalin-like an
22	18	75.0	4	3	AAP20216	Analgesic and neur
23	18	75.0	4	5	AAP40411	Chromogenic serine
24	18	75.0	4	12	AAR10140	Synthetic neurotra
25	18	75.0	4	13	AAR22254	Peptide for bindin
26	18	75.0	4	13	AAR22255	Peptide for bindin
27	18	75.0	4	13	AAR22256	Peptide for bindin
28	18	75.0	4	13	AAR22765	Leucine-enkephalin

ALIGNMENTS

RESULT 1
AAR99475
ID AAR99475 standard; peptide; 4 AA.
XX
AC AAR99475;
XX
DT 03-MAR-1997 (first entry)
XX
DE Encoded reaction cassette substrate, S1/S2.
XX
KW Encoded reaction cassette; assay; cleavage reaction; solid matrix;
KW cleavable substrate; polynucleotide; encoding sequence; primer;
KW polymerase chain reaction; detection; cleavage agent; protease;
KW catalytic activity; antibody; catalyst; diagnostic reagent; design.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 3
FT /note= "opt. D-form residue (S2)"
XX
PN WO9622391-A1.
XX
PD 25-JUL-1996.
XX
PF 18-JAN-1996; 96WO-US00888.
XX
PR 18-JAN-1995; 95US-0374050.
XX
PA (SCRI) SCRIPPS RES INST.
XX
PI Fenniri H, Janda KD, Lerner RA;
XX
DR WPI; 1996-354547/35.
XX
PT Encoded reaction or ligation cassette for assay of cleavage or
PT ligation reactions - comprises solid matrix carrying substrate
PT linked to PCR-detectable oligomer or reactant that can ligate to
PT second reactant bound to oligomer
XX
PS Example; Fig 4; 128pp; English.
XX

CC A novel encoded reaction cassette (ERC) for assaying a cleavage
CC reaction, comprises a solid matrix, a substrate (cleavable in the
CC reaction) covalently bound to the matrix (i.e. the present peptide)
CC and a 1st polynucleotide, linked to the substrate that includes an
CC encoding sequence (ES) flanked by PCR primers. The ERC is used to
CC detect cleavage agents, esp. proteases, or to assay the catalytic
CC activity of antibodies or new catalysts, esp. for diagnostic
CC reagent design.
CC To detect a cleavage agent, the test sample is incubated with ERC
CC to produce a mixt. of cleavage prods. and unreacted ERC. The
CC soluble prod. is sepd., bound polynucleotide in it amplified by PCR
CC and the amplified sequence detected.
XX
SQ Sequence 4 AA;

Query Match 100.0%; Score 24; DB 17; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGFG 4
||||
Db 1 ggfg 4

RESULT 2
AAY04398
ID AAY04398 standard; peptide; 4 AA.
XX
AC AAY04398;
XX
DT 25-JUN-1999 (first entry)
XX
DE Spacer peptide #1.
XX
KW Spacer; medicine complex; carboxyl-4C alkyl pullulan polyalcohol;
KW tumour.
XX
OS Synthetic.
XX
PN JP11092405-A.
XX
PD 06-APR-1999.
XX
PF 19-SEP-1997; 97JP-0254780.

XX
PR 19-SEP-1997; 97JP-0254780.
XX
PA (DAUC) DAIICHI PHARM CO LTD.
PA (DDSK-) DDS KENKYUSHO KK.
XX
DR WPI; 1999-283504/24.
XX
PT New medicine complex comprising pullulan alcohol - useful for its
PT tumour site selectivity
XX
PS Claim 10; Page 2; 12pp; Japanese.
XX
CC The present invention describes a medicine complex comprising a
CC carboxy1-4C alkyl pullulan polyalcohol combined with the residue of a
CC medical compound through a spacer consisting of an amino acid or a
CC spacer especially of 2 to 8 amino acids peptide-bonded. Also described
CC are: (1) a carrier for medicine delivery for combining a medical
CC compound consisting of a carboxy1-4C alkyl pullulan polyalcohol; and (2)
CC use of a carboxy1-4C alkyl pullulan polyalcohol for the preparation of a
CC medicine complex containing a carboxy1-4C alkyl pullulan polyalcohol
CC combined to the residue of a medical compound optionally through a
CC spacer. The medicine complex is useful for its tumour site selectivity.
CC The present sequence represents a specifically claimed spacer peptide.
XX
SQ Sequence 4 AA;

Query Match 100.0%; Score 24; DB 20; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGFG 4
||||
Db 1 ggfg 4

RESULT 3
AAY91118
ID AAY91118 standard; peptide; 4 AA.
XX
AC AAY91118;
XX
DT 06-OCT-2000 (first entry)
XX

DE Drug delivery system compound N-terminal tetrapeptide #1.
XX
KW Drug delivery system; DDS; saccharide; peptidase; cytostatic;
KW antiinflammatory; modified carboxy 1-4C alkyldextran polyalcohol;
KW hydrolysate; antitumour; liver cancer.
XX
OS Unidentified.
XX
PN WO200025825-A1.
XX
PD 11-MAY-2000.
XX
PF 29-OCT-1999; 99WO-JP06016.
XX
PR 30-OCT-1998; 98JP-0310130.
PR 19-NOV-1998; 98JP-0329272.
XX
PA (DAUC) DAIICHI PHARM CO LTD.
XX
PI Susaki H, Inoue K, Kuga H, Ikeda M, Shiose Y, Korenaga H;
XX
DR WPI; 2000-365409/31.
XX
PT New drug delivery system compounds comprise saccharide compound
PT modified carboxy alkyldextran polyalcohol bonded to antitumor or
PT antiinflammatory agent -
XX
PS Claim 33; Page 52; 64pp; Japanese.
XX
CC The present invention describes a drug delivery system (DDS) compound
CC comprising a saccharide compound modified carboxy 1-4C alkyldextran
CC polyalcohol bonded to a drug compound. Also described is a method of
CC assaying DDS compounds with a drug bonded to a polymer carrier via a
CC spacer containing 2-8 amino acids, comprising assaying a hydrolysate
CC obtained by treating the DDS compound with a peptidase. The compound
CC is used as a drug delivery system for administering e.g. antitumour
CC and antiinflammatory drugs, especially for treating liver cancer. The
CC assay can be used to monitor distribution and blood levels of the drug
CC to allow accurate dosing. The carrier increases bioavailability of drug
CC and allows the drug levels in the body to be readily assayed. The
CC present sequence represents a specifically claimed N-terminal
CC tetrapeptide which is used in the exemplification of the present
CC invention.
XX
SQ Sequence 4 AA;

Query Match 100.0%; Score 24; DB 21; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGFG 4
||||
Db 1 ggfg 4

RESULT 4
AAY49436
ID AAY49436 standard; peptide; 4 AA.
XX
AC AAY49436;
XX
DT 17-MAR-2000 (first entry)
XX
DE Spacer peptide molecule in a drug composite.
XX
KW Drug composite; spacer; drug delivery system; antitumor;
KW antiinflammatory.
XX
OS Synthetic.
XX
PN WO9961061-A1.
XX
PD 02-DEC-1999.
XX
PF 21-MAY-1999; 99WO-JP02681.
XX
PR 22-MAY-1998; 98JP-0140915.
XX
PA (DAUC) DAIICHI PHARM CO LTD.
XX
PI Susaki H, Inoue K, Kuga H;
XX
DR WPI; 2000-072550/06.
XX
PT Drug composite comprises carrier bound to drug via spacer useful as
PT drug delivery systems -
XX
PS Claim 16; Page 41; 53pp; Japanese.
XX
CC The invention provides drug composites comprising a polymer carrier

CC bound through an amino acid spacer to a drug. The drug composite
CC comprises a compound of formula A-R-NH-Y-CH2-O-CO-Q where, A = polymer
CC carrier for a drug; R = spacer comprising 1-8 amino acid molecules bound
CC to each other through a peptide linkage; Y = optionally substituted
CC phenylene; Q = residue of drug. The drug composites are used as drug
CC delivery systems for antitumor or antiinflammatory agents. The composites
CC give rapid and regioselective release of drug thus increasing activity
CC and maximum tolerated dose of drug. The present sequence represents a
CC spacer peptide of the drug composite.
XX
SQ Sequence 4 AA;

Query Match 100.0%; Score 24; DB 21; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGFG 4
||||
Db 1 ggfg 4

RESULT 5
AAY04402
ID AAY04402 standard; peptide; 5 AA.
XX
AC AAY04402;
XX
DT 25-JUN-1999 (first entry)
XX
DE Spacer peptide #5.
XX
KW Spacer; medicine complex; carboxyl-4C alkyl pullulan polyalcohol;
KW tumour.
XX
OS Synthetic.
XX
PN JP11092405-A.
XX
PD 06-APR-1999.
XX
PF 19-SEP-1997; 97JP-0254780.
XX
PR 19-SEP-1997; 97JP-0254780.
XX

PA (DAUC) DAIICHI PHARM CO LTD.
PA (DDSK-) DDS KENKYUSHO KK.
XX
DR WPI; 1999-283504/24.
XX
PT New medicine complex comprising pullulan alcohol - useful for its
PT tumour site selectivity
XX
PS Disclosure; Page 6; 12pp; Japanese.
XX
CC The present invention describes a medicine complex comprising a
CC carboxy1-4C alkyl pullulan polyalcohol combined with the residue of a
CC medical compound through a spacer consisting of an amino acid or a
CC spacer especially of 2 to 8 amino acids peptide-bonded. Also described
CC are: (1) a carrier for medicine delivery for combining a medical
CC compound consisting of a carboxy1-4C alkyl pullulan polyalcohol; and (2)
CC use of a carboxy1-4C alkyl pullulan polyalcohol for the preparation of a
CC medicine complex containing a carboxy1-4C alkyl pullulan polyalcohol
CC combined to the residue of a medical compound optionally through a
CC spacer. The medicine complex is useful for its tumour site selectivity.
CC The present sequence represents an example of a spacer peptide given in
CC the present invention.
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 24; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGFG 4
||||
Db 2 ggfg 5

RESULT 6
AAB03528
ID AAB03528 standard; Protein; 5 AA.
XX
AC AAB03528;
XX
DT 06-OCT-2000 (first entry)
XX
DE Drug delivery system compound peptide #4.
XX

KW Drug delivery system; DDS; saccharide; peptidase; cytostatic;
KW antiinflammatory; modified carboxy 1-4C alkyldextran polyalcohol;
KW hydrolysate; antitumour; liver cancer.
XX
OS Unidentified.
XX
PN WO200025825-A1.
XX
PD 11-MAY-2000.
XX
PF 29-OCT-1999; 99WO-JP06016.
XX
PR 30-OCT-1998; 98JP-0310130.
PR 19-NOV-1998; 98JP-0329272.
XX
PA (DAUC) DAIICHI PHARM CO LTD.
XX
PI Susaki H, Inoue K, Kuga H, Ikeda M, Shiose Y, Korenaga H;
XX
DR WPI; 2000-365409/31.
XX
PT New drug delivery system compounds comprise saccharide compound
PT modified carboxy alkyldextran polyalcohol bonded to antitumor or
PT antiinflammatory agent -
XX
PS Disclosure; Page 14; 64pp; Japanese.
XX
CC The present invention describes a drug delivery system (DDS) compound
CC comprising a saccharide compound modified carboxy 1-4C alkyldextran
CC polyalcohol bonded to a drug compound. Also described is a method of
CC assaying DDS compounds with a drug bonded to a polymer carrier via a
CC spacer containing 2-8 amino acids, comprising assaying a hydrolysate
CC obtained by treating the DDS compound with a peptidase. The compound
CC is used as a drug delivery system for administering e.g. antitumour
CC and antiinflammatory drugs, especially for treating liver cancer. The
CC assay can be used to monitor distribution and blood levels of the drug
CC to allow accurate dosing. The carrier increases bioavailability of drug
CC and allows the drug levels in the body to be readily assayed. The
CC present sequence represents a peptide which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 24; DB 21; Length 5;

Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGFG 4
||||
Db 2 ggfg 5

Search completed: July 12, 2002, 14:20:50
Job time: 89 sec